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, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.
 Creation of genome-wide protein expression libraries using random activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@atersys.com
 High quality sequence stop: 499.
 Location/Qualifiers
 1..807
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="H1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT 211 a 195 c 178 g 222 t
 ORIGIN

Alignment Scores:
 Pred. No.: 6.04e-102 Length: 807
 Score: 1002.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-895-298a-83 (1-190) x BG184448 (1-807)

QY 1 MetMetAsnPhcInProProSerLysAlaTrpArgAlaSerGlnMetThrPhe 20
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 DB 85 ATGATGATTTCAGCTCGAGCAAAAGCTGGGGCCACAGATGATGATTTCTTC 144
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
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 DB 145 ATCTTCTGCTTTTCCATCTTCACCGGGGCTCTTGCGACCTGGCCATCACCATC 204
 QY 41 TrpArgLeuLysProSerAlaAspGlyLysProPheArgGlyLeuProLeuPheIleHis 60
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 DB 205 TGGAGATTGAAGCTTCAGCTGACTGGCCCTTTTCGAGGTCTGCTCTTCATTCAC 264
 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
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 DB 265 TCATCTACAGCTGATCGACACCCCTAAGTACACGGCGCTGCTGCTGGTGGTGG 324
 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
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 DB 325 ATCTATCGGAACCTCATGTGAAAGTGTGCACTTTTTCATCTCACCCTCATTTGCTA 384
 QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyArgGlyIleMetIleArgLeuLeu 120
 |||||||
 DB 385 ATCATACCTATCTTACCTGCGAGATCACAGAGGAAGATATGATGAAGGCTGCTC 444
 QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspIleMetPheLeuIleGlnLysLeuIleLys 140
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 DB 445 CAGACACAGATCTTATATAGGGCAAGATAATTTCTCTGATATAAAAAATTGATCAAG 504
 QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgArgGlnVal 160
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 DB 505 CTCACAGATATGAGAAAGAAAGCAACCCAGCTCACTTCTTGAAAGAGAGGAGG 564
 *QY 161 GlnGlnGlnGlyPheLeuHisLeuGlnGlyLysAspGlySerLeuAspLeuArgSerArg 180
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 DB 565 GAGCAACAAGGGCTTTTGGATTGGGGGAACATGATGGCAGTCTTGACTTGGATCTAGA 624

QY 181 ArgSerValGlnGlnLysProArgAla 190
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 DB 625 AGATCAGTTCACAGAGTATATCAAGGCC 654

RESULT 2
 BG217799
 LOCUS BG217799 777 bp mRNA linear EST 21-APR-2001
 DEFINITION R3737513 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
 ACCESSION BG217799
 VERSION BG217799.1 GI:13743820
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 777)
 Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.
 Creation of genome-wide protein expression libraries using random activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@atersys.com
 High quality sequence stop: 512.
 Location/Qualifiers
 1..777
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="H1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT 196 a 193 c 173 g 214 t
 ORIGIN

Alignment Scores:
 Pred. No.: 9.87e-101 Length: 777
 Score: 991.00 Matches: 188
 Percent Similarity: 98.95% Conservative: 0
 Best Local Similarity: 98.95% Mismatches: 2
 Query Match: 98.90% Indels: 0
 DB: 12 Gaps: 0

US-09-895-298a-83 (1-190) x BG217799 (1-777)

QY 1 MetMetAsnPhcInProProSerLysAlaTrpArgAlaSerGlnMetThrPhe 20
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 DB 85 ATGATGATTTCAGCTCGAGCAAAAGCTGGGGCCACAGATGATGATTTCTTC 144
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
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 DB 145 ATCTTCTGCTTTTCCATCTTCACCGGGGCTTTTGCACTTGGCCATCACCATC 204
 QY 41 TrpArgLeuLysProSerAlaAspGlyLysProPheArgGlyLeuProLeuPheIleHis 60
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 DB 205 TGGAGATTGAAGCTTCAGCTGACTGGCCCTTTTCGAGGTCTGCTCTTCATTCAC 264
 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
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 DB 265 TCATCTACAGCTGATCGACACCCCTAAGTACACGGCGCTGCTGCTGGTGGTGG 324

OY		81	IleTTTAAAGANLeuIIeGLySeValHisShePhePheIleuThLeuIIeValLeu	100
Db		325	ATCTATCGGAACCTCATTTGCAAGTGTCACACTTTTTCATCTCACCCTACTGTGCTA	384
OY		101	IleIleThrTYrLeuTYrTrpGlnIlleHrGlueJLarqLySIleMetIleArgLeuLeu	120
Db		385	ATCATCACCCATTACTTACTGGCAGATGCACAGAGAAGGAAGATTAATGAGGCTGTC	444
OY		121	HISglunilIleIleasnGlUGlyLYAsplysmethPeuIleGIUlysLeuIIeLys	140
Db		445	CATGACGCCAATCATTAAGAGGGCAAAGATAAATGTCTCCATGAGAAAATTTGATCAAG	504
OY		141	LengInAspmEtGILySLySAlAsmProSerSerIleValIIeugLnArqGluval	160
Db		505	CTCGACGAGTATGGAGAACAAAGCAACCCCACGCTCCTGTTCTTGAAAGAGAGAGGTG	564
OY		161	GIUnGInGnIlyPheLeuHISLeuGIlyLuHISAspGIySerLeuAspLeuARgSerArq	180
Db		565	GAGACAACAAGSCTTTTTTCATTTGGGGGACATGATGCAGCTTGACTTGCGATCTANA	624
OY		181	ArgSerValGInGInGlyAsnProArgAla	190
Db		625	AGATCATGTTCACAAAGAGTAATCCAAAGGCC	654
RESULT		3		
LOCUS		AM582253	691 bp	mRNA linear EST 16-MAR-2000
DEFINITION		OYA-STO212-120100-075-f09	STO212 Homo sapiens cDNA,	mRNA sequence.
ACCESSION		AM582253		
VERSION		AM582253.1	GI:7257302	
KEYWORDS		EST.		
SOURCE		human.		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 691) HGCP http://www.ludwig.org.br/ORESTES. The FAPESP/LICR Human Cancer Genome Project Unpublished (1999)		
AUTHORS		Contact: Simpson A.J.G.		
TITLE		Laboratory of Cancer Genetics		
JOURNAL		Ludwig Institute for Cancer Research		
COMMENT		Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-7704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2-QVA-STO212- 120100-075-f09&t3=2000-01-12&t4=1) Seq primer: puc 18 forward High quality sequence start: 5 High quality sequence stop: 667. Location/Qualifiers 1..691 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_id="STO212" /dev_stage="Adult" /note="Organ: stomach; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) Profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
FEATURES				
source				
BASE COUNT		179 a	167 c	157 g 188 t
ORIGIN				
Alignment Scores:		1.71e-98	Length:	691
Pred. NO.:				

Percent Similarity:	970.50	Matches:	189
Score:	99.47%	Conservative:	1
Best Local Similarity:	99.47%	Mismatches:	1
Query Match:	96.86%	Indels:	0
DB:	10	Gaps:	1
US-09-895-298A-83 (1-190) x AWS82253 (1-691)			
QY 1 MetMetAsnPhgInProProSerIysAlaTriPaGalAsSerGImeMetThrPhe	20		
Db 28 ATGATGAATTTCCACCCTCCGAGCA - GCCTGGCGGGCTCACAGATGATGCTTTCTTC	85		
QY 21 IlePheIleuPhePheProSerPheThrGlyValIleuCysThrIleuAlaIleThrIle	40		
Db 86 ATCTCTTGCTCTTTTCCATCTTCACCCGGGGCTTTGTGACCTTGCCATCCACATC	145		
QY 41 TriPaGLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis	60		
Db 146 TGGAAATTTGAACCTTCACGTACGTGTGGCCCTTTTCGAGGTCTCCCTCTTCAATTCAC	205		
QY 61 SerIleYrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTriPaValTrp	80		
Db 206 TCCATCTACAGCTGGATCGACACCTAAGTACACGGCTGGCTTACCTGTGGCTTTGG	265		
QY 81 IleTyrArgAsnIleIleGlySerValHisPhePhePheIleLeuThrIleValIleu	100		
Db 266 ATCTATCGGAACCTCATTTGGAAGTGTGACCTTTTTCATCTTCACCTCATTTGTGCTA	325		
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyIleArgLysIleMetIleArgPheLeu	120		
Db 326 ATCATCACCTATCTTTACTGGCAGATCACAGAGGAGAGAGATTAATGTAAGCTGCTC	385		
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys	140		
Db 386 CATGACGAGATCATTAATGAGGAGCAAGATAAATGTTCCGTATGAAATAATGATCAAG	445		
QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerIleValIleGlnArgGluVal	160		
Db 446 CTGCAGGATATGTGAAAGAAAGCAACCCACAGCTCATCTTGTCTGAAAGGAGACAGGTG	505		
QY 161 GlnGlnGlnGlyPheLeuHisIleuGlnGlyHisAspGlySerLeuAspLeuArgSerArg	180		
Db 506 GAGCAACAAGGCTTTTGGATTGGGGGAACATGATGGCAGTCTTGACTTGGCATCTAGA	565		
QY 181 ArgSerValGlnGlnGlyLysAsnProArgAla	190		
Db 566 AGATCAGTTCAAGAAAGTAAATCCAAAGGCC	595		
RESULT 4			
LOCUS	BGI194960	768 bp	mRNA linear EST 21-APR-2001
DEFINITION	R5114018 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BGI194960		
VERSION	BGI194960.1	GI:13716535	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 768)		
JOURNAL	Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,		
MEDLINE	Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,		
COMMENT	Lerner, L., Costanzo, D., McEllisott, K., Booser, S., Mays, R., Smith		
	, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher		
	, J., Danzig, J. and Ducar, M.		
	Creation of genome-wide protein expression libraries using random		
	activation of gene expression		
	Nat. Biotechnol. 19 (5), 440-445 (2001)		
	21227151		
	Contact: Scott J. Cain		
	Athersys, Inc.		
	3201 Carnegie Ave, Cleveland, OH 44115, USA		
	Tel: 216 431 9900		

Fax: 216 361 9596
Email: scai@atherys.com
High quality sequence stop: 469.
Location/Qualifiers

FEATURES
1. 768
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 197 a 188 c 171 g 212 t
ORIGIN

Alignment Scores:

Pred. No.: 6.26e-97 Length: 768
Score: 957.00 Matches: 185
Percent Similarity: 97.89% Conservative: 1
Best Local Similarity: 97.37% Mismatches: 4
Query Match: 95.51% Indels: 1
DB: 12 Gaps: 0

US-09-895-298a-83 (1-190) x BG2194960 (1-768)

QY 1 MetMetAspPheGlnProProSerLysAlaTrpArgAlaSerGlnMetThrPhePhe 20
DB 85 ATCATGAAATTTCCAGCCTCCGAGCAAGCCTGGGCGCTCACAGATGATCTTCTTC 144
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
DB 145 ATCTTCTGCTCTTTTCCATCTTCACCGGGGCTGTGAGCACCCTGGGCATCACCATC 204
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
DB 205 TGGAGATTGAAAGCCTTCAGCTGAGCTGGCCCTTTTCGAGTCTGCCTCTTCATTCAC 264
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
DB 265 TCCATCTACAGCTGATCGACACCCCTTAAGTACACGGCCTGGCTAAGCTGGGTTGTTGG 324
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
DB 325 ATCTATCGGAACCTCATGTGGAAGTGCACCTCTTTTATCTCTCAACCTCATTTGCTCA 384
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyArgLysIleMetIleArgLeuLeu 120
DB 385 ATCATCACCCTATCTTACTGGCAGATCACAGAGGAAGATTAATGATTAAGGCTGCTC 444
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
DB 445 CATGACGACATCTTATATGAGGCAAGATTAATGTTCTCTGATAGAAATTTGATCAAG 504
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGlnLysArgGluVal 160
DB 505 CTCGACGATATGAGGAAGAAAGCAACCCAGCTCACTTGCTGGAAGAGAGAGGTC 564
QY 161 GlnGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArgSerArg 180
DB 565 GACCAACAAGGCTTTTGGCTTTGGGGGGAACATGATGGCAGTTTGATCTTGATCTAAG 624
QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
DB 625 AGACA-CTTCAGAGAGCTATCCAGAGGCC 653

RESULT 5
LOCUS BG221275 789 bp mRNA linear EST 21-APR-2001
DEFINITION RST1079 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG221275

VERSION BG221275.1 GI:13747296
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Homo sapiens
1 (bases 1 to 769)
Harrington,J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.
Created by genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE
JOURNAL
MEDLINE
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atherys.com
High quality sequence stop: 533.
Location/Qualifiers

FEATURES
source
1. 789
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 191 a 194 c 171 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 4.15e-93 Length: 789
Score: 923.00 Matches: 183
Percent Similarity: 96.34% Conservative: 1
Best Local Similarity: 95.81% Mismatches: 6
Query Match: 92.12% Indels: 2
DB: 12 Gaps: 0

US-09-895-298a-83 (1-190) x BG221275 (1-789)

QY 1 MetMetAspPheGlnProProSerLysAlaTrpArgAlaSerGlnMetThrPhePhe 20
DB 188 ATCATGAAATTTCCAGCCTCCGAGCTAAGCCTGGGCGCTCACAGATGATCTTCTTC 247
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
DB 248 ATCTTCTGCTCTTTTCCATCTTCACCGGGGCTGTGAGCACCCTGGGCATCACCATC 307
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
DB 308 TGGAGATTGAAAGCCTTCAGCTGAGCTGGCCCTTTTCGAGTCTGCCTCTTCATTCAC 367
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
DB 368 TCCATCTACAGCTGATTCACACCCCTTAAGTACACGGCCTGGCTAAGCTGGGTTGTTGG 427
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
DB 428 ATCTATCGGAACCTCATGTGGAAGTGCACCTTTTATCTCTCAACCTCATTTGCTCA 487
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyArgLysIleMetIleArgLeuLeu 120
DB 488 ATCATCACCCTATCTTACGCGAGATCACAGAGGAAGATTAATGATTAAGGCTGCTC 547
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140

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Db 548 CATGAGCATCATTAATGAGGCAAGATAAATGTTCCGTAGAGAAAATGATGACAG 607
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Qy 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160
|||||
Db 608 CTGCAGGATATGAGAAAGAAAGCAAGCCAGCCACTGTTGTCGANAAGAGAGNACTG 667
|||
Qy 161 GluGlnGlnGlyPheLeuHisLeuGluGluHisAspGlySerLeuAspLeuArgSerArg 180
|||||
Db 668 GAGNCACAGAGCTTTTTCATTTGNG-GAACATGATGGCACTTTCGACTTCGATCTAGA 726
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Qy 181 ArgSerValGlnGluGly-AsnProArgAla 190
|||||
Db 727 AGATCAGTTCAAGAGGTAATCCAGGGCC 757
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RESULT 6
Bg216071 837 bp mRNA linear EST 21-APR-2001
LOCUS Bg216071
DEFINITION RST35885 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION Bg216071
VERSION Bg216071.1 GI:13742220
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 837)
AUTHORS Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,D., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
JOURNAL MEDLINE
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
Location/Qualifiers
High quality sequence stop: 537.
FEATURES
SOURCE 1..837
Location/Qualifiers
1..837
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 208 a 209 c 184 g 235 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 4,51e-92 Length: 837
Score: 914.00 Matches: 182
Percent Similarity: 96.84% Conservative: 2
Best Local Similarity: 95.79% Mismatches: 6
Query Match: 91.22% Indels: 2
DB: 12 Gaps: 0
US-09-895-298a-83 (1-190) x Bg216071 (1-837)
Qy 1 MetMetAspPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
Db 124 ATGATGAATTTCCACGCTCCGAGCAAGCTGGCGGCTCCACAGATGATGACTTTCTTC 183
Qy 21 IlePheLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40

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Qy 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
|||||
Db 244 TGGAGATTGAAGCCCTTCAGCTGAGCTGCCCTTTTTCAGAGGTGCTCCCTTCATTCAC 303
|||||
Qy 61 SerIleYrSerTrpIleAspThrLeuSerThrArgProGlyTrpLeuTrpValValTrp 80
|||||
Db 304 TCCATCTACACTGGATGACACCCCTAAGTACAGGCGCTGGCTACCTGTGGGTGTGG 363
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Qy 81 IleTrpArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
|||||
Db 364 ATCATATCGAAGACATATGGAAGTGTGCACTTTTTCATCTCCTACCCCTCATTTGTGCTA 423
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Qy 101 IleIleThrTrpLeuTrpTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
|||||
Db 424 ATCATACACCTATCTTTACTGTCAGATCACAGAGGGAAGATTAATGATGAAGCTGCTC 483
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Qy 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
|||||
Db 484 CATGAGCATCATTAATGAGGCAAGATAAATGTTCTGTATGAAAATGTATCAAG 543
|||||
Qy 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
|||||
Db 544 CTGCAGGATATGAGAAAGAAAGCAAGCCAGCTCAGTCTGTTTCGANAAGAGAGAGGTG 603
|||||
Qy 161 GluGlnGlnGlyPheLeuHisLeuGluGluHisAspGlySerLeuAspLeuArgSerArg 180
|||||
Db 604 GAGCA-CAGAGCTTTTTCATTTGGGGGACATGAGGCGAG-CTTGACTTGGAGTCTAGA 661
|||||
Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190
|||||
Db 662 AGATCAGCTCAAGAGGTGATCCAGGGCC 691
|||||

RESULT 7
Bg183902 823 bp mRNA linear EST 21-APR-2001
LOCUS Bg183902
DEFINITION RST2815 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION Bg183902
VERSION Bg183902.1 GI:13705589
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 823)
AUTHORS Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,D., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
JOURNAL MEDLINE
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
Location/Qualifiers
High quality sequence stop: 449.
FEATURES
SOURCE 1..823
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation

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method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 211 a 203 c 180 g 229 t

ALIGNMENT SCORES:

Pred. No.: 3 48e-91 Length: 823
Score: 906.00 Matches: 183
Percent Similarity: 96.34% Conservative: 1
Best Local Similarity: 95.81% Mismatches: 6
Query Match: 90.42% Indels: 3
DB: 12 Gaps: 0

US-09-895-298a-83 (1-190) x BG183902 (1-823)

QY 1 MetMetAspNheGlnProProSerLysAlaTPrpArgAlaSerGlnMetMetThrPhePhe 20
|||||
DB 109 ATGATGAATTTCCAGCCTCGAGCAAGCCTGGCGGCTCCACAGATGATGACTTTCTTC 168
QY 21 IlePheLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
|||||
DB 169 ATCTTCTGCTCTTTTCCATCTTCACCGGGGCTTGTCACCCCTGGCCATCACCATC 228
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
|||||
DB 229 TGGAGATGGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGCTGCTCTTCATTCAC 288
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyTrpLeuTrpValValTrp 80
|||||
DB 289 TCCATCTACAGCTGATCGACACCCCTAAGTACACGGCTGGCTGGCTGGCTGGCTGG 348
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
|||||
DB 349 ATCTATCGGAACCTCAATGGAGAGTGTGCACTCTTTTTCATCTTCACCCCTCATTTGTCTA 408
QY 101 IleIleThrTyTrpLeuTyTrpGlnIleThrGlnGlyArgLysIleMetIleArgLeuLeu 120
|||||
DB 409 ATCATACCTATCTTACTTACGGCAGATCACAGAGGAAGATTTGTATGAAGCTGTCTC 468
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys 140
|||||
DB 469 CAGACACACATCATCTATGAGGCAAGATTAATATCTCTGATGAAAAATGATCAAG 528
QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgArgGluVal 160
|||||
DB 529 CTCGAGATATATGAGAAATATAGCAACCCACGCTCACTTGTCTGAAAGAGAGAGGG 588
QY 161 Gln-GlnGlnGlyPheLeuHisLeuGlnHisAspGlySerLeuAspLeuArgSerArg 180
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DB 589 GAAGCAACAAGGCTTTTTCATTTGGGGAAACATGATGACAGTCTTGACTT-CGATCTAA 647
QY 180 gArgSerValGlnGlnGlyLysAsnProArgAla 190
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DB 648 AATATCAGTTCAAGAAAGGAT-CCAAAGGGCC 677

RESULT 8
BG217267 810 bp mRNA linear EST 21-APR-2001
LOCUS BG217267
DEFINITION R3736969 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG217267
VERSION BG217267.1 GI:13743288
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 810)
Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cald,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothran,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.

TITLE
Creation of genome-wide protein expression libraries using random

JOURNAL
MEDLINE
COMMENT
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@athersys.com
High quality sequence stop: 466.
Location/Qualifiers

FEATURES
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1..810
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="see 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, In press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT 207 a 196 c 180 g 227 t

ALIGNMENT SCORES:

Pred. No.: 9.6e-91 Length: 810
Score: 902.00 Matches: 177
Percent Similarity: 95.26% Conservative: 4
Best Local Similarity: 93.16% Mismatches: 7
Query Match: 90.02% Indels: 2
DB: 12 Gaps: 0

US-09-895-298a-83 (1-190) x BG217267 (1-810)

QY 1 MetMetAspNheGlnProProSerLysAlaTPrpArgAlaSerGlnMetMetThrPhePhe 20
|||||
DB 85 ATGATGAATTTCCAGCCTCGAGCAAGCCTGGCGGCTCCACAGATGATGACTTTCTTC 144
QY 21 IlePheLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
|||||
DB 145 ATCTTCTGCTCTTTTCCATCTTCACCGGGGCTTGTCACCCCTGGCCATCACCATC 204
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
|||||
DB 205 TGGAGATGGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGCTGCTCTTCATTCAC 264
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyTrpLeuTrpValValTrp 80
|||||
DB 265 TCCATCTACAGCTGATCGACACCCCTAAGTACACGGCTGGCTGGCTGGCTGGCTGG 324
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
|||||
DB 325 ATCTATCGGAACCTCAATGGAGAGTGTGCACTCTTTTTCATCTTCACCCCTCATTTGTGCTA 384
QY 101 IleIleThrTyTrpLeuTyTrpGlnIleThrGlnGlyArgLysIleMetIleArgLeuLeu 120
|||||
DB 385 ATCATACCTATCTTACTTACGGCAGATCACAGAGGAAGATTTGTATGAAGCTGTCTC 444
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys 140
|||||
DB 445 CATGACACATCATTAATAGGCAAGATTAATATGCTCTGATGAAAAATGATCAAG 504
QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgArgGluVal 160
|||||
DB 505 CTCGAGATATATGAGCAAGCAAGCAAGCCTGCTCTTGTCTGAAAGAGAGAGG 564
QY 161 GlnGln-GlnGlyPheLeuHisLeu-GlyLysHisAspGlySerLeuAspLeuArgSerArg 180
|||||
DB 565 GAAGCAACAAGGCTTTTTCATTTGGGGAAACATGATGACAGTCTTGACTTGGCATCTA 624
QY 180 gArgSerValGlnGlnGlyLysAsnPro 188
|||||

Db	625	GAATTCATTCAGAGGATCCCA	650
RESULT 9			
AK016573			
LOCUS	AK016573	2721 bp	mRNA
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932443l08:homolog to CDNA FLJ13593 FIS, CLONE PLCEI009493, full insert sequence.		
ACCESSION	AK016573		
VERSION	AK016573.1	GI:12855380	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library clone:4932443l08.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-Format		
JOURNAL	Sequencing pipeline with 384 multichipillary sequencer		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nakado, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carinici, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, K., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085660		
PUBMED	11217851		
REFERENCE	5 (bases 1 to 2721)		
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Aikawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirooka, T., Horii, F.,		
FEATURES	<p>source</p> <p>CDs</p> <p>polyA_signal</p> <p>polyA_site</p>		
COMMENT	<p>Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Ow, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamana, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.</p> <p>Direct Submission</p> <p>Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suhei-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)</p> <p>Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.</p> <p>cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adaptor of sequence [5' GAGAGAGAGATTCGAGTAAATTAATTCACCCGCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised between 3 and 7 kb was selected before cloning. Vector: a modified phuescript KS(+) after bulk excision from lambda phage I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.</p> <p>Location/Qualifiers</p> <p>1..2721</p> <p>/organism="Mus musculus"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="FANTOM_DB:4932443l08"</p> <p>/db_xref="MGI:1907597"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="4932443l08"</p> <p>/sex="male"</p> <p>/tissue_type="testis"</p> <p>/clone.lib="RIKEN full-length enriched mouse cDNA library"</p> <p>/dev_stage="adult"</p> <p>/note="data source:SPRR, source key:09H817, evidence:ISS homolog to CDNA FLJ13593 FIS, CLONE PLCEI009493</p> <p>putative</p> <p>/codon_start=1</p> <p>/protein_id="BAB30314.1"</p> <p>/db_xref="GI:12855381"</p> <p>/db_xref="MGI:1921674"</p> <p>/translation="MOSDQVDEIIIEVENPSSQVNHVSSQILAKSSANPARCVLSSAADRDCQIFNPGNDRNRRLRFSSLNLSISQIHGSECLVDSCTFHEHCVGSSALDLPMTTRIRIKTRINQPRMQKRELKATYDEKKNQSGILLEANCAACGSSILTRTRNGLSELNLYITLMQRFYVIGGFSTVLSYSPFLMLKFNIFEVMNSFLITFOEYVAGAKNTLOFTLEFFTGAGYGVGMVYMGYSPTNIRRMGASVMOLAVFTTGACIVCFPSLSPMAKYPFNNPHTYSGAKLFCMDPFTYHKAVKLQKNLSTEIRENSELKRENYRTFNOULTRSAHYAAVSYGVCYACCAVAYYLAEYNSFLKTRNPGAVLLPVPVSCINLAVRYSMRFLVETIPROEVYLLVRLNIFLKISVIGILCYWNLINVALSGECWETLLIGDYLIRLMDPVSILADSLGELRLIGMKFTSISLOEPDIARNVALIELIAQTLTWGIFCCLPFIOMITLFIEMFYAVNSLMANPOPSKARASOMTTFEFLFPEFSTVCLTIAITIRLPSADCGPGLSPFOSISYMDITLSRRPGYLVWVYIOMLIGSVHFFIITLIVLITTYLWOTTECKVMIRLHEQIINGKRMFLIEKTLQDMKEKYNVNSALDPERREVPQIPLHBEIGAAPDLKRSAGDENPIA"</p> <p>2702..2707</p> <p>/note="putative"</p> <p>2721</p>		

BASE COUNT 678 a 692 c 644 g 707 t

ORIGIN

Alignment Scores:

Pred. No.:	4,08e-85	Length:	2721
Score:	857.00	Matches:	166
Percent Similarity:	90.53%	Conservative:	6
Best Local Similarity:	87.37%	Mismatches:	18
Query Match:	85.53%	Indels:	0
DB:	11	Gaps:	0

US-09-895-298a-83 (1-190) x AK016573 (1-2721)

QY 1 MetMetAsnPhcInPrProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
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 DB 1908 ATATGACTTCCAGCCCAAGCAAGCCCTGGCGGCTCAGAGATGATTAATCTTCTTC 1967
 |||||
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrIleuAlaIleThrIle 40
 |||||
 DB 1968 ATTTCTGTGCTTCTTCCATCTTCACAGGAGTGCTGTGACACCTGGCTATCACATC 2027
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 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 |||||
 DB 2028 TGGAGACTGAAACCTTCGGCTGACTGTGGCCCTCCGAGGCTGCTCCCTTCATCCAA 2087
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 QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValIleTrp 80
 |||||
 DB 2088 TCATGTACAGCTGTGATGTGACATCTGAGCCGAGGCTGTACTGTGGTGGTCTGG 2147
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 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrIleValLeu 100
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 DB 2148 ATCTACAGAAATCTCATGTGAAAGTGACACTTCTTCTTCACTCCATTCATTTGGCTA 2207
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 QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyArgGlyIleMetIleArgLeuLeu 120
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 DB 2208 ATATGACTATCTTCTTACGTGGAGATCAGAGAGGGGAGAGGTGATTCATTTGCTC 2267
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 QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
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 DB 2268 CAGCAACAGATCTTATATGAGGCAAGATATATGTCTCTGATAGAAATTTGACCMAA 2327
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 QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGluVal 160
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 DB 2328 CTACAGAGATTTGGAGAGAGATCAACCCAGTGCCTTACCTGAAAGAGAGAGGTG 2387
 |||||
 QY 161 GlnGlnGlnGlyPheLeuHisLeuGlnHisAspGlySerLeuAspLeuArgSerArg 180
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 DB 2388 GAGCCCAAAATTCCTTTGCACTTTGGAGAACTTGTGTCTCTCTGACCTTGATGGAG 2447
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 QY 181 ArgSerValGlnGlnLysAsnProArgAla 190
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 DB 2448 CGGTCAAGCAAGAGAGAAATCCCATAGCC 2477
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 RESULT 10
 BE375244 698 bp mRNA linear EST 24-NOV-2000
 LOCUS QV4-ST0212-261199-045-c09 ST0212 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE375244
 ACCESSION BE375244
 VERSION BE375244.1 GI:11337269
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 698)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
 Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,
 Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare,
 M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
 Simpson, A. J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL
 MEDLINE
 20202663
 COMMENT

sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-ST0212-261199-045-c09&t3=1999-11-26&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 36.
 Location/Qualifiers

FEATURES

source

1..698
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ST0212"
 /dev_stage="Adult"
 /note="Organ: stomach; Vector: puc18; Site_1: Sma1;
 Site_2: Sma1; A mini-library was made by cloning products
 derived from ORESPES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 177 a 173 c 164 g 184 t

ORIGIN

Alignment Scores:

Pred. No.:	2.46e-79	Length:	698
Score:	799.50 <td>Matches:</td> <td>163 </td>	Matches:	163
Percent Similarity:	90.22% <td>Conservative:</td> <td>3 </td>	Conservative:	3
Best Local Similarity:	88.59% <td>Mismatches:</td> <td>16 </td>	Mismatches:	16
Query Match:	79.79% <td>Indels:</td> <td>3 </td>	Indels:	3
DB:	12	Gaps:	1

US-09-895-298a-83 (1-190) x BE375244 (1-698)

QY 9 LysAlaTrpArgAlaSerGlnMet---MetThrPhePheIlePheLeuPhePhe 27
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 DB 55 CAAGCTGGGGGGCTTAACAGACTGATAGACTTTGATATCTTCTTGTCTATTTTCC 114
 |||||
 QY 27 oSerPheThrGlyValLeuCysThrIleuAlaIleThrIleTrpArgLeuLysProSerAl 47
 |||||
 DB 115 ATCTTACACCGGGGCTGTGGACCCCTGGCCATCAGATCGAGATTGAAGCTTCACC 174
 |||||
 QY 47 aaSPcysGlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAs 67
 |||||
 DB 175 TGACTGTGGCCCTTTTCAGAGCTGCTGCTCTTCATTCATCTCATCTACAGCTGATGCA 234
 |||||
 QY 67 pThrLeuSerThrArgProGlyTyrLeuTrpValIleTrpIleTyrArgAsnLeuIleG 87
 |||||
 DB 235 CACCCTAAGTACAGGCGCTGGCTACTGTGGGTTGTTGGATGTATGGAACCTCATTTGG 294
 |||||
 QY 87 ySerValHisPhePheIleLeuThrIleuValLeuIleIleThrTyrLeuTyrTrp 107
 |||||
 DB 295 AAGTGTGCACTTCTTTTATCTCAACCCGATGCTATGCTATCATCAGCATATCTTACTG 354
 |||||
 QY 107 pGlnIleThrGlyArgGlyIleMetIleArgLeuLeuHisGlnGlnIleIleAsnGln 127
 |||||
 DB 355 GCAGATCACAGAGAGAGAGATCATGATCAGAGCTGCTCCATGAGCAGATCATTTATGA 414
 |||||
 QY 127 uGlyLysAspLysMetPheLeuIleGlyLysLeuIleLysLeuGlnAspMetGlnLysLys 147
 |||||
 DB 415 GGGCAAGCATCAATGTCTCTGATAGAAACATTGATGATCAAGCTCAGAGATATGGCAGCAG 474
 |||||
 QY 147 salaAsnProSerSerLeuValLeuGlnLysArgGluValGlnGlnGlnGlyPheLeuH 167

Db	475	CGCAAAACCAGC-TACTGTGACGTGAAGAAGAGAGTGGAGCAACAAGGCTTTATTCOA	533
Oy	167	sleuclygluhisapglyserleuaspleunargSerarArgSerValGlnGluGlyAs	187
Db	534	TTAGCGGGACATCATGTGCAGCTGTGACTTGCGATCTAGACGATCATGTTCAAGAAGCTAA	593
Oy	187	nproArghla 190	
Db	594	TTCAAAGGGCC 603	
RESULT 11	BG219307	822 bp	mRNA linear EST 21-APR-2001
LOCUS	BG219307		
DEFINITION	R5339601 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BG219307		
VERSION	BG219307.1	GI:13745328	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 822) Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J , Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith ,E., Veloso,N., Kilka,A., Hess,J., Colchen,K., Lo,K., Offendacher ,J., Dandig,J. and Ducar,M. Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)		
AUTHORS	21227151		
JOURNAL	Contact: Scott J. Cain		
MEDLINE	Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scaine@atersys.com		
COMMENT	High quality sequence stop: 473. Location/Qualifiers 1..822 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology', in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."		
FEATURES	BASE COUNT 241 a 169 c 179 g 230 t		3 others
SOURCE	ORIGIN		
	Alignment Scores:		
	Pred. No.:	1.63e-76	Length: 822
	Score:	775.00	Matches: 148
	Percent Similarity:	100.00%	Conservative: 0
	Best local Similarity:	100.00%	Mismatches: 0
	Query Match:	77.35%	Indels: 0
	DB:	12	Gaps: 0
US-09-895-298A-83	(1-190) x BG219307	(1-822)	
Oy	43	LeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIle	62
Db	79	TTGAAGCCTTCAGCTGACGATGAGGCCCTTTGCAAGCTGCTGCTCTTCATTCACTTCATC	138
Oy	63	TyrSerTrpIleAspThrLeuSerThraArgProGlyTyrLeuTrpValValTrpIleTyr	82
Db	139	TACAGCTGGATGCAGACACCTAGTACAGAGCGCTGCTACTGTGGGTGTTTGGAGTCAAT	198
Oy	83	ArgasnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeuIleIle	102

Db	199	CGAAGCCATTTGGAAAGTGTGACCTCTTTTTCATCCACACCCCTATTGTGTATCATTC	258
QY	103	ThrTyrLeuTyrTrpGlnIleThrgluGlyArgLysIleMetIleArgLeuLeuHsclu	122
Db	259	ACCTATCTTTACTGTGCACATCACAGAGGGAAGGAAGATTATGATGAAGCTGCTGCATGAG	318
QY	123	GlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLysLeuGln	142
Db	319	CAGATCATTAATGAGGGGCAAGATATAAATGTCCGATGAGAAAAAATTAATCAAGTGCAG	378
QY	143	AspMetGluLysLysAlaAsnProSerSerLeuValIleGluArgArgGluValGluGln	162
Db	379	GATATGGAGGAAGAAAGCAACACCCAGCTCCTCTTGTTCGAAAGAGAGAGTGGAGCAA	438
QY	163	GlnGlyPheLeuHsLsLeuGlyLysIleHsAspGlySerLeuAspLeuArgSerArgArgSer	182
Db	439	CAAGCCTTTTTCGATTTTGGGGAGCATGATGACAGTCTTGACTTCGATCTGATGAAGATCA	498
QY	183	ValGlnGluGlyAsnProArgAla	190
Db	499	GTTCAAGAAAGGTAATCCAAAGGGCC	522
RESULT 12			
LOCUS	BG198917	871 bp	mRNA linear EST 21-APR-2001
DEFINITION	RS1818188 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BG198917		
VERSION	BG198917.1	GI:13720604	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 871) Harrington,J.J. to Shif		
TITLE	Cain,S., Leventhal,C., Thornton,M., Ramchandran R., Whittington,J., Lerner,L., Cosanzo,D., McElligott,K., Booser,S., Mays,R., Smith ,E., Veloso,N., Kliska,A., Hess,J., Colhren,K., Lo,K., Offenbacher ,J., Danzig,J. and Ducar,M.		
JOURNAL MEDLINE	Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)		
COMMENT	21272151 Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scaine@atersys.com High quality sequence stop: 498.		
FEATURES	Location/Qualifiers		
source	1..871 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology. In press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."		
BASE COUNT	252 a 186 c 185 g 246 t		2 others
ORIGIN			
Alignment Scores:			
Pred. No.:	1.08e-74	Length:	871
Score:	759.00	Matches:	146
Percent Similarity:	98.65%	Conservative:	0
Best Local Similarity:	98.65%	Mismatches:	2
Query Match:	75.75%	Indels:	0
DB:	12	Gaps:	0

US-09-895-298a-83 (1-190) x BG198917 (1-871)

QY 43 LeuYsProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIle 62
 |||||||
 Db 117 TTGAAGCTTCACAGTACGCTGAGCCCTTTTCGAGGCTGCTCTCTCATTCACCTCATC 176
 |||||||
 QY 63 TyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIleTyr 82
 |||||||
 Db 177 TACAGTGGATGACACCCCTTAAGTACAGCGCTGCTACCTGGGTGGTGGATCTAT 236
 |||||||
 QY 83 ArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrIleValIleIleIle 102
 |||||||
 Db 237 TGAACCTCAATGGAATGTCACCTCTTTTTCATCTCACTCCATTCATGCTAATATC 296
 |||||||
 QY 103 ThrTyrLeuTyrTrpGlnIleThrGlnGlyIleArgIleMetIleArgLeuIleHisGln 122
 |||||||
 Db 297 ACCTATCTTACTGCGCATGACAGAGAGAAAGAGATTTGATTAAGCTGCTCCATGAG 356
 |||||||
 QY 123 GlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleTyrLeuGln 142
 |||||||
 Db 357 CAGATCATTAATGAGGCAAGATAAATGTTCTCTGATAGAAAATGATCAAGCTGCAG 416
 |||||||
 QY 143 AspMetLysLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnValGlnGln 162
 |||||||
 Db 417 GATATGGAAGAGAAAGCAACCCAGCTCACTTCTGAAAGAGAGAGGAGAGCAAA 476
 |||||||
 QY 163 GlnGlyPheLeuHisLeuGlnGlyLysAspGlySerLeuAspLeuArgSerArgSer 182
 |||||||
 Db 477 CAAGGCTTTTGCATTTGGGGGGAACATGATGCGATCTTACTTGGATTCAGATCA 536
 |||||||
 QY 183 ValGlnGlnLysAsnProArgAla 190
 |||||||
 Db 537 GTTCAAGAAAGTAAATCCAGAGGCC 560
 |||||||

RESULT 13
 BG982234/c 447 bp mRNA linear EST 12-JUN-2001

LOCUS
 DEFINITION CM4-CN0089-130201-723-e04 CN0089 Homo sapiens cDNA, mRNA sequence.
 BG982234
 ACCESSION
 VERSION BG982234.1 GI:14384969
 KEYWORDS
 SOURCE EST.
 ORGANISM human.
 Homo sapiens
 Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 447)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brustein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 CONTACT: Simpson A.J.G.
 LABORATORY: Laboratory of Cancer Genetics
 LUDWIG INSTITUTE FOR CANCER RESEARCH
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4<2=CM4-CN0089-
 130201-723-e04<3=2001-02-13<4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 25
 Location/Qualifiers

source

1. .447
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CN0089"
 /dev_stage="Adult"
 /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent Application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 114 a 107 c 95 g 131 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2 12e-67 Length: 447
 Score: 691.00 Matches: 133
 Percent Similarity: 99.25% Conservative: 0
 Best Local Similarity: 99.25% Mismatches: 1
 Query Match: 68.96% Indels: 0
 DB: 13 Gaps: 0

US-09-895-298a-83 (1-190) x BG982234 (1-447)

QY 57 LeuPheIleHisSerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeu 76
 |||||||
 Db 446 CTCTTATTCACATCCATCACTACAGCTGATGACACCCCTTAAGTACAGCGCTGACTACTG 387
 |||||||
 QY 77 TrpValValTrpIleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThr 96
 |||||||
 Db 386 TGGGCTGTTTGGATCTATCGGAACCTCATGGAAGTGTGCACTTCTTTCATCCCTCAC 327
 |||||||
 QY 97 LeuIleValLeuIleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgLysIleMet 116
 |||||||
 Db 326 CTCAATTTGCTTAATCATCACTACCTTATCTTACTGCGAGATCCACAGAGAGAAAGATTAATG 267
 |||||||
 QY 117 IleArgLeuLeuHisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGln 136
 |||||||
 Db 266 ATTAAGGCTGCTCCATGACAGCATCATTAATGAGGGCAAGATAAATGTTCTGATAGAA 207
 |||||||
 QY 137 LysLeuIleLysLeuGlnAspMetGlnLysAlaAsnProSerSerLeuValLeuGln 156
 |||||||
 Db 206 AAATTTGATCAAGCTGCGAGGTATGAGAGAAAGCAACCCAGCTCACTTGTCTGGAA 147
 |||||||
 QY 157 ArgArgGlnValGlnGlnGlnGlyPheLeuHisLeuGlnLysAspGlySerLeuAsp 176
 |||||||
 Db 146 AGGAGAGAGGTGAGACACAAAGGCTTTTTCATTTGGGGGAACATATGTCAGCTTGAC 87
 |||||||
 QY 177 LeuArgSerArgArgSerValGlnGlnGlnLysAsnProArgAla 190
 |||||||
 Db 86 TTGCGATCTGAAGATCAGTTCAAGAGGTAAATCCAAAGAGGCC 45
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RESULT 14
 BG198969 758 bp mRNA linear EST 21-APR-2001

LOCUS
 DEFINITION RST18241 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 BG198969
 ACCESSION
 VERSION BG198969.1 GI:13720656
 KEYWORDS
 SOURCE EST.
 ORGANISM human.
 Homo sapiens
 Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 758)
 Harrington,J.J., Sherif,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
 E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher,
 J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 552.
Location/Qualifiers
1..758
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 172 a 193 c 163 g 229 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2.32e-66 Length: 758
Score: 684.00 Matches: 143
Percent Similarity: 94.90% Conservative: 6
Best Local Similarity: 91.08% Mismatches: 8
Query Match: 68.26% Indels: 3
Gaps: 0
US-09-895-298a-83 (1-190) x BG198969 (1-758)
QY 1 MetMetAnpMegInPrProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
DB 284 ATGATGAAATTCACACCTCCAGCAAAAGCTGGCGGCTCAGATGATGACTTCTTC 343
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
DB 344 ATCTTCTTGCTCTTTTCCATCTTCACCGGGCTTGTCACCCCTGGCCATCCATC 403
QY 41 TrpArgLeuLysProSerAlaAPcysGlyProPheArgGlyLeuProLeuPheIleHis 60
DB 404 TGGAGATTGAAGCCTTCACTGACGTGAGCCCTTTTCAGAGCTCTCTCTCATTTCA 463
QY 61 SerIleTyTrSerTrpIleAspThrIleuSerThrArgProGlyTyTrLeuTrpValIleTrp 80
DB 464 TCCATCTACAGCTGGATGACACCTTAAGTACACGCGCTGCTACCTGGGTTGTTGG 523
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValIleu 100
DB 524 ATCTTCCGAAACCTCATTTGGAAGTGTGCACTTCTTCTCCCTCACTCATTTGTGCTA 583
QY 101 IleIleThrTyTrLeuTyTrPheGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
DB 584 ATCATCACCTATCTTACTTGGCAGATCAAGAGGGAAGATATGATTAAGCTGTGCTC 643
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys 140
DB 644 CTTAG-CAGATCATTTGATGAGGCAAAATTAATGTCTCGATCGAATA-ATGATCAAG 701
QY 141 LeuGlnAPMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArg 157
DB 702 CTGCGAGTATGACACAAAGACACCCCACTTA-CTAGTTTCTGGAAGA 751
RESULT 15
AW469181/c 594 bp mRNA linear EST 24-FEB-2000
LOCUS hc78f11.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2898861 3'
DEFINITION similar to TR:043284 043284 IAK-4P.; mRNA sequence.
ACCESSION AW469181
VERSION AW469181.1 GI:7039287
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 594)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: www-bio.llnl.gov/dbfp/image/image.html
Seq primer: -40up from Gibco
High quality sequence stop: 404.
Location/Qualifiers
1..594
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2898861"
/clone_lib="NCI-CGAP-Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: PCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.65 kb. Life Technologies catalog #: 11349-011"
BASE COUNT 161 a 139 c 108 g 186 t
ORIGIN
Alignment Scores:
Pred. No.: 4.78e-54 Length: 594
Score: 573.00 Matches: 113
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 57.19% Indels: 0
Gaps: 0
US-09-895-298a-83 (1-190) x AW469181 (1-594)
QY 77 TrpValValTrpIleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThr 96
DB 594 TGGGTGTTGGAATGATTCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATCCATCACC 535
QY 97 LeuIleValLeuIleIleThrTyTrLeuTyTrGlnIleThrGlnGlyArgGlyIleMet 116
DB 534 CTCAATTGGCTAATCATCATCTTACTTGGCAGATCACAGAGGAAGATTAAG 475
QY 117 IleArgLeuLeuHisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGln 136
DB 474 ATTAAGCTGCTCATGAGACATCATTAATGAGGCAAGAAATGATGCTGTGTAAGA 415
QY 137 LysLeuIleLysLeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGln 156
DB 414 AAATTGATCAACCTCGAGATATGGAAGAAAGCAAAACCCAGCTCACTTCTTGGA 355
QY 157 ArgArgGlnValGlnGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAsp 176
DB 354 AGGAGAGAGGTGAGACACAAAGGCTTTTGTGATTTGGGGGAGACATGATGAGCTGTGAC 295
QY 177 LeuArgSerArgArgSerValGlnGlnGlnGlyAsnProArgGala 190
DB 294 TTGCGATCTAGAAAGATCAGTTCAAGAGGATTAATCCAAAGGCC 253
Search completed: November 9, 2002, 06:12:16

Tue Nov 12 15:09:10 2002

us-09-895-298a-83.rst

Page 12

Job time : 2206 secs
